

## BLAST

### Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

#### Protein Sequence (19 letters)

residues 2-20 of SEQ ID No: 13

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

#### Query ID

|cl|45680

|cl|45680

#### Description

None

#### Molecule type

amino acid

#### Query Length

19

#### Database Name

nr

#### Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

#### Program

BLASTP 2.2.22+ [Citation](#)

#### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Multiple alignment](#) [NEW](#)

### Search Parameters

Program	blastp
Word size	2
Expect value	200000
Hitlist size	100
Gapcosts	9,1
Matrix	PAM30
Threshold	11
Filter string	F
Genetic Code	1
Window Size	40

### Database

Posted date	Jan 5, 2010 4:42 AM
Number of letters	3,507,711,756
Number of sequences	10,280,272
Entrez query	none

**Karlin-Altschul statistics**

Params	Ungapped	Gapped
Lambda	0.368935	0.294
K	0.285947	0.11
H	1.85525	0.61

**Results Statistics**

Length adjustment	9
Effective length of query	10
Effective length of database	3415189308
Effective search space	34151893080
Effective search space used	34151893080

Graphic Summary

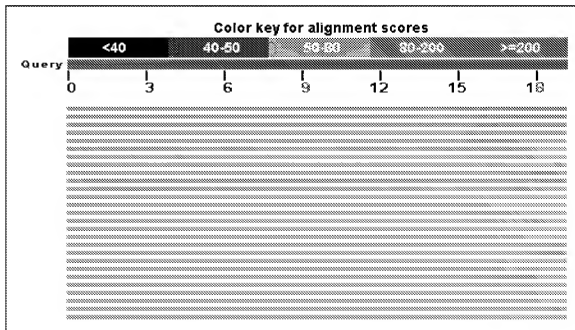
Show Conserved Domains

Hit the button to

**See conserved domains from CDD****Distribution of 100 Blast Hits on the Query Sequence**

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



[illegible]

## Descriptions

E	Sequences producing significant alignments:	Score	
		(Bits)	Value
gb AAN59509.1	HBsAg [Hepatitis B virus]	55.4	7e-07
gb EAG06746.1	hepatitis B surface antigen [Hepatitis B virus]	51.5	1e-05
gb A080319.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACQ82752.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACQ82751.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACQ82750.1	large S protein [Hepatitis B virus]	50.7	2e-05
dbj BAH84151.1	hepatitis B surface antigen [Hepatitis B virus]	50.7	2e-05
dbj BAH82937.1	hepatitis B surface antigen [Hepatitis B virus]	50.7	2e-05
dbj BAH82930.1	hepatitis B surface antigen [Hepatitis B virus]	50.7	2e-05
gb ACJ66246.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66247.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66243.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66241.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66240.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66233.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66229.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66227.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66226.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66213.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66212.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66207.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66206.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66205.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66186.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66185.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66184.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66164.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66163.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66136.1	middle S protein [Hepatitis B virus] >gb ACJ66...	50.7	2e-05
gb ACJ66135.1	large S protein [Hepatitis B virus] >gb ACJ661...	50.7	2e-05
gb ACJ66130.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66129.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66128.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66122.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66096.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66095.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66081.1	large S protein [Hepatitis B virus] >gb ACJ660...	50.7	2e-05
gb ACJ66090.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66093.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66094.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66097.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66096.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66059.1	S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66058.1	middle S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66057.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66190.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66182.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66190.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66170.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66160.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66154.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66138.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66134.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66123.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66097.1	large S protein [Hepatitis B virus] >gb ACJ661...	50.7	2e-05
gb ACJ66094.1	large S protein [Hepatitis B virus]	50.7	2e-05
gb ACJ66086.1	large S protein [Hepatitis B virus]	50.7	2e-05

gb ACR65020.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACR65064.1	large S protein [Hepatitis B virus]	>gb ACR661...	50.7	2e-05
gb ACR65064.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65043.1	large S protein [Hepatitis B virus]	>gb ACR659...	50.7	2e-05
gb ACR65041.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65032.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACR65021.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACR65003.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65004.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACR65000.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACR65076.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65069.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65059.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACR65055.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65052.1	large S protein [Hepatitis B virus]	>gb ACR659...	50.7	2e-05
gb ACR65040.1	large S protein [Hepatitis B virus]	>gb ACR660...	50.7	2e-05
gb ACR65033.1	large S protein [Hepatitis B virus]	>gb ACR658...	50.7	2e-05
gb ACR65025.1	large S protein [Hepatitis B virus]	>gb ACR658...	50.7	2e-05
gb ACR65017.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65009.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR65007.1	large S protein [Hepatitis B virus]	>gb ACR658...	50.7	2e-05
gb ACR60704.1	S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60703.1	middle S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60700.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60564.1	S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60563.1	middle S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60560.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60447.1	truncated large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60413.1	S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60412.1	middle S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60411.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60326.1	S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60325.1	middle S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60324.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60320.1	S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60319.1	middle S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60318.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60311.1	S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60310.1	middle S protein [Hepatitis B virus]		50.7	2e-05
gb ACR60309.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR603730.1	large S protein [Hepatitis B virus]		50.7	2e-05
gb ACR603726.1	large S protein [Hepatitis B virus]		50.7	2e-05

Alignments Select All Get selected sequences Distance tree of results Multiple alignment NEW

>gb|AAX59509.1| HBsAg [Hepatitis B virus]  
Length=101

Score = 55.4 bits (123), Expect = 7e-07  
Identities = 18/19 (94%), Positives = 18/19 (94%), Gaps = 0/19 (0%)

Query 1 GSTRSTGQCKTCTTAAQG 19  
GST TSTGQCKTCTTAAQG  
Sbjct 1 GSTRSTGQCKTCTTAAQG 19

>dbj|BAG06746.1| hepatitis B surface antigen [Hepatitis B virus]  
Length=132

Score = 51.5 bits (114), Expect = 1e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRSTGQCKTCTTAAQG 19  
GST TSTG CKTCTTAAQG

Sbjct 73 GSTTTSTGCKTCTTPAQQ 91

>gb|ADB03191.1| large S protein [Hepatitis B virus]  
Length=400

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 286 GSTTTSTGPKCTCTTPAQQ 304

>gb|ACQ82752.1| S protein [Hepatitis B virus]  
Length=226

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 112 GSTTTSTGPKCTCTTPAQQ 130

>gb|ACQ82751.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 167 GSTTTSTGPKCTCTTPAQQ 185

>gb|ACQ82750.1| large S protein [Hepatitis B virus]  
Length=400

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 286 GSTTTSTGPKCTCTTPAQQ 304

>dbj|BAH84154.1| hepatitis B surface antigen [Hepatitis B virus]  
Length=132

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 73 GSTTTSTGPKCTCTTPAQQ 91

>dbj|BAH83937.1| hepatitis B surface antigen [Hepatitis B virus]  
Length=132

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 73 GSTTTSTGPKCTCTTPAQQ 91

>dbj|BAH83930.1| hepatitis B surface antigen [Hepatitis B virus]  
Length=132

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 73 GSTTTSTGPKCTCTTPAQQ 91

>gb|ACJ66248.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 167 GSTTTSTGPKCTCTTPAQQ 185

>gb|ACJ66247.1| large S protein [Hepatitis B virus]  
Length=400

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 286 GSTTTSTGPKCTCTTPAQQ 304

>gb|ACJ66242.1| S protein [Hepatitis B virus]  
Length=226

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 112 GSTTTSTGPKCTCTTPAQQ 130

>gb|ACJ66241.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 167 GSTTTSTGPKCTCTTPAQQ 185

>gb|ACJ66240.1| large S protein [Hepatitis B virus]  
Length=400

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 286 GSTTTSTGPKCTCTTPAQQ 304

>gb|ACJ66233.1| large S protein [Hepatitis B virus]  
Length=400

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 286 GSTTTSTGPKCTCTTPAQQ 304

>gb|ACJ66228.1| S protein [Hepatitis B virus]  
Length=226

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAQQ 19  
GST TSTG CKTCTTPAQQ  
Sbjct 112 GSTTTSTGPKCTCTTPAQQ 130

>gb|ACJ66227.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 167 GSTTTSTGPKCTCTTPAAG 185

>gb|ACJ66226.1| large S protein [Hepatitis B virus]  
Length=400

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 286 GSTTTSTGPKCTCTTPAAG 304

>gb|ACJ66213.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 167 GSTTTSTGPKCTCTTPAAG 185

>gb|ACJ66212.1| large S protein [Hepatitis B virus]  
Length=400

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 286 GSTTTSTGPKCTCTTPAAG 304

>gb|ACJ66207.1| S protein [Hepatitis B virus]  
Length=226

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 112 GSTTTSTGPKCTCTTPAAG 130

>gb|ACJ66206.1| middle S protein [Hepatitis B virus]  
Length=279

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 165 GSTTTSTGPKCTCTTPAAG 183

>gb|ACJ66205.1| large S protein [Hepatitis B virus]  
Length=398

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 284 GSTTTSTGPKCTCTTPAAG 302

>gb|ACJ66186.1| S protein [Hepatitis B virus]  
Length=226

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)



Query 1 GSTRISTGQCKTCTTPAAG 19  
 Sbjct 112 GSTTTSTGPKCTCTTPAAG 130

>gb|ACJ66185.1| middle S protein [Hepatitis B virus]  
 Length=281

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
 Sbjct 167 GSTTTSTGPKCTCTTPAAG 185

>gb|ACJ66184.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
 Sbjct 286 GSTTTSTGPKCTCTTPAAG 304

>gb|ACJ66164.1| middle S protein [Hepatitis B virus]  
 Length=281

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
 Sbjct 167 GSTTTSTGPKCTCTTPAAG 185

>gb|ACJ66163.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
 Sbjct 286 GSTTTSTGPKCTCTTPAAG 304

>gb|ACJ66136.1| middle S protein [Hepatitis B virus]  
 gb|ACJ66178.1| middle S protein [Hepatitis B virus]  
 gb|ACJ66192.1| middle S protein [Hepatitis B virus]  
 gb|ACJ66198.1| middle S protein [Hepatitis B virus]  
 Length=281

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
 Sbjct 167 GSTTTSTGPKCTCTTPAAG 185

>gb|ACJ66135.1| large S protein [Hepatitis B virus]  
 gb|ACJ66177.1| large S protein [Hepatitis B virus]  
 gb|ACJ66191.1| large S protein [Hepatitis B virus]  
 gb|ACJ66203.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
 Sbjct 286 GSTTTSTGPKCTCTTPAAG 304

>gb|ACJ66130.1| S protein [Hepatitis B virus]  
 Length=226

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
 GST TSTG CKTCTTPAAG  
 Sbjct 112 GSTTTSTGPKCTCTTPAAG 130

>gb|ACJ66129.1| middle S protein [Hepatitis B virus]  
 Length=281

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
 GST TSTG CKTCTTPAAG  
 Sbjct 167 GSTTTSTGPKCTCTTPAAG 185

>gb|ACJ66128.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
 GST TSTG CKTCTTPAAG  
 Sbjct 286 GSTTTSTGPKCTCTTPAAG 304

>gb|ACJ66122.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
 GST TSTG CKTCTTPAAG  
 Sbjct 286 GSTTTSTGPKCTCTTPAAG 304

>gb|ACJ66096.1| S protein [Hepatitis B virus]  
 Length=226

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
 GST TSTG CKTCTTPAAG  
 Sbjct 112 GSTTTSTGPKCTCTTPAAG 130

>gb|ACJ66095.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
 GST TSTG CKTCTTPAAG  
 Sbjct 286 GSTTTSTGPKCTCTTPAAG 304

>gb|ACJ66081.1| large S protein [Hepatitis B virus]  
 >gb|ACJ66088.1| large S protein [Hepatitis B virus]  
 >gb|ACJ66142.1| large S protein [Hepatitis B virus]  
 >gb|ACJ66156.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRISTGQCKTCTTPAAG 19  
 GST TSTG CKTCTTPAAG  
 Sbjct 286 GSTTTSTGPKCTCTTPAAG 304

>gb|ACJ66006.1| S protein [Hepatitis B virus]  
 Length=226

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 112 GSTTTSTGPKCTCTTPAAG 130

>gb|ACJ66005.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 167 GSTTTSTGPKCTCTTPAAG 185

>gb|ACJ66004.1| large S protein [Hepatitis B virus]  
Length=400

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 286 GSTTTSTGPKCTCTTPAAG 304

>gb|ACJ65907.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 167 GSTTTSTGPKCTCTTPAAG 185

>gb|ACJ65906.1| large S protein [Hepatitis B virus]  
Length=400

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 286 GSTTTSTGPKCTCTTPAAG 304

>gb|ACJ65859.1| S protein [Hepatitis B virus]  
Length=226

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 112 GSTTTSTGPKCTCTTPAAG 130

>gb|ACJ65858.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAAG 19  
GST TSTG CKTCTTPAAG  
Sbjct 167 GSTTTSTGPKCTCTTPAAG 185

>gb|ACJ65857.1| large S protein [Hepatitis B virus]  
Length=400

Score = 50.7 bits (112), Expect = 2e-05  
Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19  
 Sbjct 286 GSTTTSTGPKCTCTTPAQG 304

>gb|ACR66198.1| large S protein [Hepatitis B virus]  
 Length=215

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19  
 Sbjct 124 GSTTTSTGPKCTCTTPAQG 142

>gb|ACR66182.1| large S protein [Hepatitis B virus]  
 Length=215

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19  
 Sbjct 124 GSTTTSTGPKCTCTTPAQG 142

>gb|ACR66180.1| large S protein [Hepatitis B virus]  
 Length=215

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19  
 Sbjct 124 GSTTTSTGPKCTCTTPAQG 142

>gb|ACR66170.1| large S protein [Hepatitis B virus]  
 Length=215

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19  
 Sbjct 124 GSTTTSTGPKCTCTTPAQG 142

>gb|ACR66160.1| large S protein [Hepatitis B virus]  
 Length=215

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19  
 Sbjct 124 GSTTTSTGPKCTCTTPAQG 142

>gb|ACR66152.1| large S protein [Hepatitis B virus]  
 Length=215

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19  
 Sbjct 124 GSTTTSTGPKCTCTTPAQG 142

>gb|ACR66138.1| large S protein [Hepatitis B virus]  
 Length=215

Score = 50.7 bits (112), Expect = 2e-05  
 Identities = 17/19 (89%), Positives = 17/19 (89%), Gaps = 0/19 (0%)

Query 1 GSTRTSTGQCKTCTTPAQG 19  
 Sbjct 124 GSTTTSTGPKCTCTTPAQG 142